



1  
SEQUENCE LISTING

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<110> Korman, Al  
Halk, Edward L.  
Lonberg, Nils  
Medarex, Inc.

<120> Human CTLA-4 Antibodies and Their Uses

<130> 014643-010510US

<140> US 09/644,668  
<141> 2000-08-24

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<160> 41

<170> PatentIn Ver. 2.1

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&lt;213&gt; Homo sapiens

&lt;220&gt;

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 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60  
  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser  
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 gacaggttca gtggcagtgg gtctggaca gacttcactc tcaccatcag cagactggag 240  
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<213> Homo sapiens

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<223> light chain variagle region predicted sequence for  
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 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
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Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
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<210> 8

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<213> Homo sapiens

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<223> light chain variable region (Vk) 4B6 from Vk A-27

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 gacaggttca gtggcagtgg gtctggaca gacttcactc tcaccatcag cagactggag 240  
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<210> 9

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<213> Homo sapiens

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<223> light chain variable region predicted sequence for  
 4B6 from Vk A-27

<400> 9

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 20 25 30

Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
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Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
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<223> Vk L-15 germline sequence

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<210> 11

<211> 94

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<213> Homo sapiens

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<223> light chain variable region predicted sequence for  
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<400> 11

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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

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70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr  
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<210> 12  
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 20 25 30

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 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

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<212> PRT

<213> Homo sapiens

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<223> heavy chain variable region predicted sequence for  
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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
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Ala Arg

<210> 16

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<212> DNA

<213> Homo sapiens

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<210> 17

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

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35 40 45Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
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&lt;210&gt; 18

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; heavy chain variable region VH 4B6 from VH 3-30.3

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&lt;210&gt; 19

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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hr Phe Ile Ser Tyr Asp Gly Ser Asn Lys His Tyr Ala Asp Ser Val			
50	55		60
ys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
55	70		75
eu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys			
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la Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr			
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Leu Val Thr Val Ser Ser  
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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
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<213> *Homo sapiens*

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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
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 85 90 95

Ala Arg

<210> 22  
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 35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Phe Tyr Cys  
 85 90 95

Ala Arg Ala Pro Asn Tyr Ile Gly Ala Phe Asp Val Trp Gly Gln Gly  
 100 105 110

Thr Met Val Thr Val Ser Ser  
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 <213> Homo sapiens  
  
 <220>  
 <223> heavy chain CDR1 (HuMab 10D1, 4B6)  
  
 <400> 27  
 Ser Tyr Thr Met His  
     1                  5

<210> 28  
 <211> 5  
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 <213> Homo sapiens  
  
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 <223> heavy chain CDR1 (HuMab 1E2)

<400> 28  
Ser Tyr Gly Met His  
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<210> 29  
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*B26*  
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<400> 30  
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<210> 31  
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<400> 31  
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<210> 32  
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<213> Homo sapiens  
  
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Gly

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<213> Homo sapiens

<220>  
<223> heavy chain CDR2 (HuMab 4B6)

<400> 33  
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Gly

<210> 34  
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<213> Homo sapiens

<220>  
<223> heavy chain CDR2 (HuMab 1E2)

<400> 34  
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Gly

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<220>  
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<400> 35  
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<212> PRT  
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<220>  
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<400> 36  
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<210> 37  
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<213> Homo sapiens

<220>

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<400> 37

Thr Gly Trp Leu Gly Pro Phe Asp Tyr

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5

<210> 38

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<223> heavy chain CDR3 (MuMab 1E2)

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Ala Pro Asn Tyr Ile Gly Ala Phe Asp Val

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chain plasmid pCK7-96 (partial)

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gtaaagcctg ggggcctaa tgagtgagct aactcacatt aattgcgttg cgctcaactgc 420  
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<212> DNA

<213> Artificial Sequence

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 chain plasmid pG4HE

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Bio  
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